Exhibit 2: ClustalW (Amino Acid) Alignment

CLUSTAL W 2.0 multiple sequence alignment

        Sequence format is Pearson
        number of seqs is: 2
        Sequence 1: SEQ147   311 aa
        Sequence 2: T_petrophila   312 aa

         comparing
        paramArg[setSeqNoRange]= off
         comparing

        Start of Pairwise alignments

        Sequences (1:2) Aligned. Score: 95
        Guide tree file created: [/ebi/extserv/clustalw-
        work/interactive/2007122119/clustalw2-20071221-19204050.dnd]

        CLUSTAL-Alignment file created   [/ebi/extserv/clustalw-
        work/interactive/2007122119/clustalw2-20071221-19204050.aln]

SEQ148   MNDLIRKYAKDQLETLKRIIEKSEGISILINGEDLSYPREVSLELPEYVEKFPPKASDVL 60
T_petrophila   MNDLIRKYAKDQLEILKRIIEKSEGISILINGEDLSYPREVSLELPEYVEKFPPKASDVL 60
                ************** **

SEQ148   EIDPEGENIGIDDIRTIKDFLNYSPELYTRKYVIVHDCERMTQQAANAFLKALEEPPEYA 120
T_petrophila   EVDPEEENIGIDEIRTIKDFLNYSPELYTRKYVIVHDCERMTQQAANAFLKTLEEPPEYA 120
                *:*** ******:**:********

SEQ148   VIVLNTRRWHYLLPTIKSRVFRVVVNVPKEFRDLVKEKIGDLWEELPLLERDFKTALEAY 180
T_petrophila   VIVLNTRHWHYLLPTIKSRVFRVVVNVPKEFRDLVKEKIGDFWEELPLLERDFKTAFEAY 180
                *******:*********************************:**************:***

SEQ148   KLGAEKLSGLMESLKVLETEKLLKKVLSKGLEGYLACRELLERFSKVESKEFFALFDQVT 240
T_petrophila   KLGAEKLSGLMESLKVLETEKLLKKALSEGLEGYLACRELLERFSKVESKEFFALFDQLT 240
                *********************** .**:*********************************:*

SEQ148   NTITGKDAFLLIQRLTRIILHENTWESVED-KSVSFLDSILRVKIANLNNKLTLMNILAI 299
T_petrophila   NTITGKDSFLLIQRLTRIVLHENTWESVEDQKSVSFLDSILRVKIANLNNKLTLMNILAI 300
                *******:*********:*********** **************************

SEQ148   HRERKRGVNAWS 311
T_petrophila   HRERKRGVNAWS 312
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